

INFORMAL SEQUENCE LISTING

SEQ ID NOs: 9598-9600 and SEQ ID NO:9611 correspond to SEQ ID NOs: 1-3 and SEQ ID NO:14 of co-pending USSN _____, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US. The SEQ ID NOs. of this co-pending application USSN _____, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US, will be renumbered in a subsequent amendment as SEQ ID NOs: 9598- 10,466. For clarity, the SEQ ID NOs. in this continuation-in-part of USSN _____, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US. are numbered sequentially starting with SEQ ID NO:10,467.

SEQ ID NO:9598

LS 1384258.1 622 bp fragment of alternatively spliced variant of SEQ ID NO: 9600

INFORMATION FOR SEQ ID NO:9598:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9598:

gcacacaaat tgacttatta gaaggcaatg tagcatcagg aaaagtagat gtgaatgaac 60
agagtggta gaggagaagt tggatgggt tgaaccttga aattaaaaat gatagaggaa 120
ttattattgg gaccgttggt aggaataatg acttttccac tgcaagactg aagatatcag 180
tgccccccta tattctgtgc aaaaggtgtc ttgactcat ccaaaaaatt gaacagttc 240
ctgtctcatg gagatctatc acaaagtctt taaatattac tacccatgaa attggccagg 300
gttaggacat tcaaattgtct ttatccacat tcctgaagga taattgttat agattcccta 360
cctccatagg aatgcttata atggattatc tatacatct ccacattccc acatttgca 420
ttagagaatg gaatcagtca aaccctgttc ccagagtttc ccttagagtt ctcaccctgtt 480
gtcttatatac catctaggaa tccccatctc taatgtaagc ttggagatcc gggccccccgg 540
gggacaggtg actgaaggac aaaaactgtat cctgctctgc tcagtggctg agggtacagg 600
aatgtcaca ttctcctggt ac

622

SEQ ID NO:9599

“Ly1448” 523 bp cDNA fragment of alternatively spliced variant of SEQ ID NO: 9600

INFORMATION FOR SEQ ID NO:9599:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9599:

ctgtcatgag gtctttcta tagccatca gtccttcac agggatattc accacccitgc 60
tctggatagg cacatggccg ttgtcagctc tacagtaata ttgcggca tcactcttt 120
tcacagctgg gatctccagc tctgctgaca gggAACGCTG ggttttcttt cccatactgg 180
ttcctgtggc ctctctgtac caggagaatg tgacattcc tgtaaaaaa gccactgagc 240
agagcaggat cagttttgt ccttcagtc cctgtccccc gggggcccg atctccaagc 300
ttacattaga gatggggatt cctagatgga tataagacaa caggtgagaa ctctaaggga 360
aactctggga acagggtttg actgattcca ttctctaatg caaaatgtgg gaatgtggag 420
attgtataga taatccatta taagcattcc tatggaggtt gggaatctat aacaattatc 480
cttcaggaat gtggataaag acatttgaat gtcctaacc tgg 523

SEQ ID NO:9600: LS 368109.1 1908 bp full-length clone

INFORMATION FOR SEQ ID NO:9600:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9600:

gacactcaac ttcacagtgc ctactgggc cagaagcaat catcttaccc caggagtcat 60
tgaggggctg ctcagcaccc ttggncacgc caccgtggcc ttattatttt gctacggcct 120
caaaagaaaa ataggaagac gttcagccag ggatccactc aggagcccttc ccagccctct 180
accccaagag ttcacccatcc tcaactcacc taccctcaggc cagctacagc ctatataatga 240
aaatgtgaat gttgttaatg gggatgaggt ttattctactg gcgtactata accagccgga 300
gcaggaatca gtacgacgac aaaccctggc gacacatatg gaggacaaga tgcagtcaact 360
gaacaggcag attcgctgac ccttgcggc ccctttctg tcttcgaagg agacagcatc 420
gttctgaaat gccaggaga acagaactgg aaaattcaga agatggctt ccataaggat 480
aacaagagt tatctgtttt caagaaaatt ctcagatttc ctatccaaa gtgcagttt 540
aagtgcacgt ggtaactatt tctgttagtac caaaggacaa ctctttctct gggataaaac 600
ttcaaatata gtaaagatta aaagtccaag gaatccccat ctctaattgtt agcttggaga 660
tccggggcccc cggggggacag gtgactgaag gacaaaaact gatcctgctc tgctcagtt 720
ctgggggtac agggaaatgtc acattctcctt ggtacagaga gcccacagga accagtatgg 780
gaaagaaaaac ccagcgttcc ctgtcagcag agctggtaga tcccagctgt gaaagagagt 840
gatgcoggca aatattactg tagagctgac aacggccatg tgcttatcca gagcaagggt 900
gtgaatatcc ctgtgagaat tccagtgctc cggccctgtcc tcacccctca ggtctccctgg 960
ggcccaaggct gcagtggggg acctgctgga gcttcaactgtt gaggccctgt agaggctctc 1020
ccccaaatctt gtaccaattt tatcatgagg atgtcaccctt tggaaacagc tcggcccttc 1080
tggaggaggg gcctccttca acctctctt gactgcagaa cattctggaa actactcctg 1140

tgaggccaac aacggcctgg gggcccagtg caggtggagg gcagtgccag gtcctccatc 1200
tcaggacctg atggctatag aaagagacct catgacagct ggagttctct ggggacctgt 1260
ttgggtcct tgcgttcaact ggggtgttgc ttgctgttgc atgccttgc ccacaagata 1320
tcaggagaaa gttctgccac taatgaaccc agaggggctt ccaggccaaa tcctcaagag 1380
ttcacctatt caagccaaac cccagacatg gaggagctgc agccacgtgt atgtcaatgt 1440
gggctctgtt gatgtggatg tggtttattc tcaggtctgg agcatgcagc agccagaaag 1500
ctcagcaaac atcaggacac ttctggagaa caaggactcc caagtcatct actcttctgt 1560
gaagaaatca taacacttgg aggaatcaga agggaaagtc aacagcaagg atggggcatc 1620
attaagactt gctataaaac cttatgaaaaa tgcttgaggc ttatcacctg ccacagccag 1680
aacgtgcctc aggaggcacc tcctgtcatt tttgtcctga tgatgttct tctccaatat 1740
cttctttac ctatcaatat tcattgaact gctgctacat ccagacactg tgcaaataaa 1800
ttatctgc taccttctct taagcaatca gtgtgtaaag atttgaggga agaatgaata 1860
agagatacaa ggtctcacct tcattctactg tgaagtgtat agaacagg 1908

SEQ ID NO:9611: Ly1448 protein

INFORMATION FOR SEQ ID NO:9611:

(a) SEQUENCE CHARACTERISTICS:

<212> PRT
<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9611:

Met	Gly	Lys	Lys	Thr	Gln	Arg	Ser	Leu	Ser	Ala	Glu	Leu	Glu	Ile	Pro
															15
5															
Ala	Val	Lys	Glu	Ser	Asp	Ala	Gly	Lys	Tyr	Tyr	Cys	Arg	Ala	Asp	Asn
															30
20															
Gly	His	Val	Pro	Ile	Gln	Ser	Lys	Val	Val	Asn	Ile	Pro	Val	Arg	Ile
															45
35															
Pro	Val	Ser	Arg	Pro	Val	Leu	Thr	Leu	Arg	Ser	Pro	Gly	Ala	Gln	Ala
															60
50															
Ala	Val	Gly	Asp	Leu	Leu	Glu	Leu	His	Cys	Glu	Ala	Leu	Arg	Gly	Ser
															80
65															
Pro	Pro	Ile	Leu	Tyr	Gln	Phe	Tyr	His	Glu	Asp	Val	Thr	Leu	Gly	Asn
															95
85															
Ser	Ser	Ala	Pro	Ser	Gly	Gly	Ala	Ser	Phe	Asn	Leu	Ser	Leu	Thr	
															110
100															
Ala	Glu	His	Ser	Gly	Asn	Tyr	Ser	Cys	Glu	Ala	Asn	Asn	Gly	Leu	Gly
															125
115															
Ala	Gln	Cys	Ser	Glu	Ala	Val	Pro	Val	Ser	Ile	Ser	Gly	Pro	Asp	Gly
															140
130															
Tyr	Arg	Arg	Asp	Leu	Met	Thr	Ala	Gly	Val	Leu	Trp	Gly	Leu	Phe	Gly
															160
145															
Val	Leu	Gly	Phe	Thr	Gly	Val	Ala	Leu	Leu	Leu	Tyr	Ala	Leu	Phe	His
															175
165															
170															

Lys Ile Ser Gly Glu Ser Ser Ala Thr Asn Glu Pro Arg Gly Ala Ser
 180 185 190
 Arg Pro Asn Pro Gln Glu Phe Thr Tyr Ser Ser Pro Thr Pro Asp Met
 195 200 205
 Glu Glu Leu Gln Pro Val Tyr Val Asn Val Gly Ser Val Asp Val Asp
 210 215 220
 Val Val Tyr Ser Gln Val Trp Ser Met Gln Gln Pro Glu Ser Ser Ala
 225 230 235 240
 Asn Ile Arg Thr Leu Leu Glu Asn Lys Asp Ser Gln Val Ile Tyr Ser
 245 250 255
 Ser Val Lys Lys Ser
 260

SEQ ID NO:10,467: Ra12-Ly1464 fusion cDNA sequence (see, Example 7)

atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
 cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggcccagat caagcttccc 120
 accgttcata tcgggcctac cgcccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
 ggcgcacgag tccaaacgcgt ggtcgggagc gtcggcggg caagtctcg 240
 ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cgccaccgcg gatggcggac 300
 ggcgttaacg ggcacatcc cggtgacgtc atctcggtga cctggcaaac caagtcggc 360
 ggcacgcgtc cagggaaacgt gacattggcc gagggacccc cgccgaatt ctccatggac 420
 atgaagctgg gctgtgtcct catggcctgg gccctctacc tttcccttgg tgtgctctgg 480
 gtggcccaga tgctactggc tgccagttt gagacgctgc agtgtgaggg acctgtctgc 540
 actgaggaga gcagctgcca cacggaggat gacttgactg atgcaaggga agctggctc 600
 caggtcaagg cctacactt cagtgaaaccc ttccacactga ttgtgtccta tgactggctg 660
 atcctccaag gtccagccaa gccagttttt gaaggggacc tgcgtgttct ggcgtgccc 720
 gcctggcaag actggccact gactcagggtg accttctacc gagatggctc agctctggg 780
 cccccccggc ctaacaggga attctccatc accgtggtaaaaaggcaga cagcgggcac 840
 taccactgca gtggcattt ccagagccct ggtcctggg tcccagaaac agcatctgtt 900
 gtggctatca cagttccaaaga actgtttcca ggcacattc tcagagctgt accctcagct 960
 gaaccccaag caggaagccc catgaccctg agttgtcaga caaagttgcc cctgcagagg 1020
 tcagctgccc gcctccttctt ctcccttctac aaggatggaa ggatagtgc aaggcagggg 1080
 ctctcctcag aattccagat cccacagct tcagaagatc actccgggtc atactgggt 1140
 gaggcagcca ctgaggacaa ccaagttgg aaacagagcc cccagctaga gatcagatg 1200
 cagggcttt ccagctctgc tgcacctccc acattgaatc cagtcctca gaaatcagct 1260
 gctccaggaa ctgctctga ggaggccctt gggcctctgc ctccggcgc aacccatct 1320
 tctgaggatc caggctttc ttctcctctg gggatgccag atcctcatct gtatcaccag 1380
 atgggccttc ttctcaaca catgcaggat gtgagagtcc tcctcggtca cctgctcatg 1440
 gagttgaggg aattatctgg ccacccggaa cctggacca caaaggctac tgctgaatag 1500

SEQ ID NO:10,468: Ra12-Ly1464 fusion amino acid sequence (see, Example 7)

Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 5 10 15

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30

Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala

35	40	45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val		
50	55	60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr		
65	70	75
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr		
85	90	95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser		
100	105	110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr		
115	120	125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Ser Met Asp Met Lys Leu Gly		
130	135	140
Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser Leu Gly Val Leu Trp		
145	150	155
Val Ala Gln Met Leu Leu Ala Ala Ser Phe Glu Thr Leu Gln Cys Glu		
165	170	175
Gly Pro Val Cys Thr Glu Glu Ser Ser Cys His Thr Glu Asp Asp Leu		
180	185	190
Thr Asp Ala Arg Glu Ala Gly Phe Gln Val Lys Ala Tyr Thr Phe Ser		
195	200	205
Glu Pro Phe His Leu Ile Val Ser Tyr Asp Trp Leu Ile Leu Gln Gly		
210	215	220
Pro Ala Lys Pro Val Phe Glu Gly Asp Leu Leu Val Leu Arg Cys Gln		
225	230	235
Ala Trp Gln Asp Trp Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly		
245	250	255
Ser Ala Leu Gly Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val		
260	265	270
Val Gln Lys Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln		
275	280	285
Ser Pro Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr		
290	295	300
Val Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala		
305	310	315
Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys Leu		
325	330	335
Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser Phe Tyr Lys Asp		
340	345	350
Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu Phe Gln Ile Pro		
355	360	365

Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys Glu Ala Ala Thr
370 375 380

Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln Leu Glu Ile Arg Val
385 390 395 400

Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro Thr Leu Asn Pro Ala Pro
405 410 415

Gln Lys Ser Ala Ala Pro Gly Thr Ala Pro Glu Glu Ala Pro Gly Pro
420 425 430

Leu Pro Pro Pro Pro Thr Pro Ser Ser Glu Asp Pro Gly Phe Ser Ser
435 440 445

Pro Leu Gly Met Pro Asp Pro His Leu Tyr His Gln Met Gly Leu Leu
450 455 460

Leu Lys His Met Gln Asp Val Arg Val Leu Leu Gly His Leu Leu Met
465 470 475 480

Glu Leu Arg Glu Leu Ser Gly His Arg Lys Pro Gly Thr Thr Lys Ala
485 490 495

Thr Ala Glu

SEQ ID NO:10,469: LS 238330.1 (see, Example 9)

<210> 4
<211> 1442
<212> DNA
<213> Homo sapiens

<400> 4
gcgtgaggca ccgcggctgg cctgagtttc ttcttaatac tgtatcacaa ttgtgggctg 60
tcttatgtgt tgatatcgat tgagctattt gaaataggaa ttgtatggg ttttattttt 120
tttgtaagg atataacaat atctacattc caaggatgtt gtgagggtttt ccatgatttt 180
gtatatgagc taatgttacc ttgaggggtt ggtgtgcatt atgttggatg attgttaattt 240
ttcagtgaa aatgtaccgt gtccctaaatt taaagacatg aaaaatatcc caagatcata 300
ctagatcata atagcaattc ctttacaaat gaattatgga ggttaactgtat ctctaacatgt 360
ttcccttcatg ttgttttaat gcacaaggc agaggatctg ctgacccttg gaaccagcgt 420
gagctaacca cgtgctatag acacttcatg gtgtcgacc cagggaaagtc aaagcgctt 480
gctccctcac tgtctgttag tcctcagcca ttgttacccc acccccccgtt gctccaaaac 540
ttgagttatt tcaaattgttt ctactgttc atctctccac tgacccactt ccagaaagcc 600
tgagagagttt cccaagatgc caccacccctt ccccaatcccc tcgcccacaga tctgtgtcta 660
tctcacactc tgtaagtgc gctttgcttc ttccctctttt gaaaagactg agaacacacaca 720
ttttaacatgtt ttagaaaaat gggcagcctt aaaaatgtac tgatcccacc gcccagtgtact 780
catgtatact ccaggctagc agacaaggcc ctttttgggtt ggcctgcttc tgggggttca 840
cagaaaccaa attactgtgg ttgcacaaaga attagcaggt catttacaaa gcagacatcc 900
cttcacccag actgtgggtt tgcatgctca ggttctcgtt ctatgagctt tgggtgcagga 960
tcattttggc tactggaaaa accatagctt attttaattt tctgggttgc aaagccacca 1020
cacgtgtggt ctgtggatga ccattgtctg cagaatgacg agaaggaaac agaatgtgg 1080
ttggggctca ggggtggccctt cccactggga gggaaaggccgg gaggggagccccc ttggccctggg 1140
ttttgacaca gcctgtgtc acagcctctc ctctcatctg catttctcgtt aaatgccttc 1200
cctgcccagt ggtgactttc cctcgtcact cctatggagt tctacctggaa gcccagccat 1260
gtgtggaaact gtgaagttt ctcctctgtta aagatgtttt aaagaaaagtc agcttctgaa 1320
atgttaacaaat gctaaccctt gctggaaaccc ttacactgaa aaataaaaaaa atcctggat gtttggaaaaaa 1380
agtttatca tggttgattt ttacactgaa aaataaaaaaa atcctggat gtttggaaaaaa 1440
aa 1442

SEQ ID NO:10,470: Ly1456P FL contig (see, Example 9)

<210> 5
<211> 1637
<212> DNA
<213> Homo sapiens

<400> 5
acccctggg ctcaagcaac gagccatcct cccgtcttag cctcccaact agctgagact 60
acaggcgtgg gtcaccacac ccagctaatt tttgtacttt ttgttagagac agggtctcac 120
catgttgcac aggctggtcc tgaactcctg ggctcaagta atctgcccac ctcagcctcc 180
caaagtgtt gggttacagg cgtgaggcac cgcggctggc ctgagttct tcttaatact 240
gtatcacaat tgtggctgt ctatgtgtt gatatcgatt gagctatgg aaataggaat 300
gttaatgggt gtattaaatt ttgttaagga tataacaata tctaccttcc aaggatgtt 360
tgaggtttc catgatttt tatatgagct aatgttacct ttgaggggtg gtgtgcatta 420
tgttggatga ttgttaaattt tcagtggaaa atgtaccgtg tcttaaattt aaagacatga 480
aaaatatccc aagatcatac tagatcataa tagcaattcc ttacaaatg aattatggag 540
gtaactgatc tctaacagtt tccttcatgt tggtttaatg cacaagggca gaggatctgc 600
tgacccttgg aaccagctg agctaaccac gtgctataga cacttcattt tgtcgcaccc 660
agggaaatca aagcgctttc ctccttcact gtctgtgagt cctcagccat tagtacccca 720
ccccccgtg ctccaaaact tgagttattt caaatgttcc tcactgttca tctctccact 780
gaccccactc cagaaagcct ggagagagtc ccaagatgcc acccaccttc cccaatccct 840
cgccacagat ctgtgtctat ctacactct gtaagtggcg ctgtgtttt tctctctttt 900
aaaagactga gaacacacat ttaacatgt tagggaaatg gggcagccca aaaaatgact 960
gatcccaccc cgagtgactc atgtatactc caggctagca gacaaggccc tttttgggtgg 1020
gcctgcttct gtgggttcac agaaaacccaa ttactgtggg ttgcaaaagaa tttagcaggc 1080
atttacaaag cagacatccc ttacaccaga ctgtgtttt gcatgcttagt gttctcagtc 1140
tatgagctt ggtgcaggat cattttggct actggaaaaa ccatacgctt ttttaaattt 1200
ctgggttcca aagccaccac acgtgtggtc tggatgac cattgtctgc agaatgacga 1260
ggaaggaaca gaatgtgggt tggggctcag ggtggccttc ccactgggag ggaaggcggg 1320
agggagccct tgccctgggt ttgacacag ctgtgtctca cagcctctcc tctcatctgc 1380
atttctcaga aatgccctcc ctgcccagt gacttcc ctgtcactc ctatggagtt 1440
ctacctggag cccagccatg tggacttac tctctgtaa agatggttt 1500
aagaaagtca gtttctgaaa tggtaacaatg ctaacccttcc ctgaaaccct gtaagaaata 1560
gccctgctga tagtttcttca gttttatcat gtttggattt tacactgaaa aataaaaaaaa 1620
tccctggatgttggaaa 1637

SEQ ID NO:10,471: Ly1456P FL contig ORF1 (see, Example 9)

<210> 6
<211> 98
<212> PRT
<213> Homo sapiens

<400> 6
Met His Lys Gly Arg Gly Ser Ala Asp Pro Trp Asn Gln Arg Glu Leu
5 10 15

Thr Thr Cys Tyr Arg His Phe Met Val Ser His Pro Gly Lys Ser Lys
20 25 30

Arg Phe Ala Pro Ser Leu Ser Val Ser Pro Gln Pro Leu Val Pro His
35 40 45

Pro Pro Leu Leu Gln Asn Leu Ser Tyr Phe Lys Cys Phe Ser Leu Phe
50 55 60

Ile Ser Pro Leu Thr Pro Leu Gln Lys Ala Trp Arg Glu Ser Gln Asp

65

70

75

80

Ala Thr His Leu Pro Gln Ser Leu Ala Thr Asp Leu Cys Leu Ser His
85 90 95

Thr Leu

SEQ ID NO:10,472: Ly1456P FL contig ORF2 (see, Example 9)

<210> 7
<211> 59
<212> PRT
<213> Homo sapiens

<400> 7
Met Phe Leu Thr Val His Leu Ser Thr Asp Pro Thr Pro Glu Ser Leu
5 10 15

Glu Arg Val Pro Arg Cys His Pro Pro Ser Pro Ile Pro Arg His Arg
20 25 30

Ser Val Ser Ile Ser His Ser Val Ser Ala Ala Leu Leu Leu Pro Leu
35 40 45

Leu Lys Arg Leu Arg Thr His Ile Leu Thr Cys
50 55

SEQ ID NO:10,473: Ly1456P FL contig ORF3 (see, Example 9)

<210> 8
<211> 84
<212> PRT
<213> Homo sapiens

<400> 8
Met Thr Ile Val Cys Arg Met Thr Arg Lys Glu Gln Asn Val Val Trp
5 10 15

Gly Ser Gly Trp Pro Ser His Trp Glu Gly Arg Arg Glu Gly Ala Leu
20 25 30

Ala Leu Gly Phe Asp Thr Ala Cys Ala His Ser Leu Ser Ser His Leu
35 40 45

His Phe Ser Glu Met Pro Ser Leu Pro Ser Gly Asp Phe Pro Ser Ser
50 55 60

Leu Leu Trp Ser Ser Thr Trp Ser Pro Ala Met Cys Gly Thr Val Lys
65 70 75 80

Phe Thr Pro Leu

SEQ ID NO:10,474: Ly1456P FL contig ORF4 (see, Example 9)

<210> 9
<211> 66
<212> PRT

<213> Homo sapiens

<400> 9
Met Trp Phe Gly Ala Gln Gly Gly Leu Pro Thr Gly Arg Glu Gly Gly
5 10 15
Arg Glu Pro Leu Pro Trp Val Leu Thr Gln Pro Val Leu Thr Ala Ser
20 25 30
Pro Leu Ile Cys Ile Ser Gln Lys Cys Pro Pro Cys Pro Val Val Thr
35 40 45
Phe Pro Arg His Ser Tyr Gly Val Leu Pro Gly Ala Gln Pro Cys Val
50 55 60
Glu Leu
65

SEQ ID NO:10,475:

GenBank clone on chromosome 15q21 clone b2265b18 (acc. no. AC008131)

see Figure 24 for sequence

SEQ ID NO:10,476

human secreted protein-encoding gene 9 cDNA clone HTOHB55 SEQ ID NO:1 (acc. no. AAH19210)

see Figure 25 for sequence

SEQ ID NO:10,477

human secreted protein-encoding gene 9 cDNA clone HTOHB55 SEQ ID NO:19 (acc. no. AAH19178) on chromosome 15q21

see Figure 26 for sequence

SEQ ID NO:10,478

lung cancer associated polynucleotide sequence SQID 265 (Genseq accession number AAF18246)

see Figure 29 for sequence

SEQ ID NO:10,479

homo sapiens Genbank clone on chromosome 17 clone RP11-956N15 (accession number AC021581)

see Figure 30 for sequence

SEQ ID NO:10,480: Template LS 1076101.8 HERV nucleotide sequence

(see, Example 11)

gccgctgccg ctccaggaga caggttccca tgcaggaatg aaagacatgg aaggaaagag 60
ggggccagc tccctgagtc ctgtgtccac cagctgctgc taaatacctc tgagaaactc 120
tgcttctatc taaggggacc tacccctctc gggaaatctca atacttggaa caagaacctc 180
ctagacggac ccttggcat aatgaattgg accaactgta gttccagga ctagagagcc 240
agcaatgcct ccatgaacaa tctcacccaa ttactctgct cagggaaacga ggttaactgat 300
ggacagccga ggcagccct tagggggctt aggcctccc tggggagcat ccctgaggcg 360
gactccggcc agcccgagtg atgcgatcca aagagcactc cccggtagga aattggcccg 420
gttggaaatgcc tcaccagagc aegtgttagc agttccctgt ggaggattaa cacagtggct 480
gaacaccggg aaggaactgg cacttggagt ccggacatct gaaacttggta gactgggagc 540
tgtacatggg tgggagcagc ttccaccaacc cctgcaaatg gactctgaaag aagacgacaa 600
gcccgtctcc agtcacacccc ggaagctgac tggccacgc acagctgaaag catgaggaaa 660
ctcatcgccg gactaatttt ccttaaaatt tagacttgca cagtaaggac ttcaactgac 720
cttcctcaga ctgagaactg ttccctgtat atacatcaag tcactgaggt aggacaaaag 780
attgctacat tcctattatt ttaaggttac atttttgggg acccctctt cttctgttct 840
agctattacc ttcttggtt caccttagaaa aggaccagtc ctaatttggta ttttaaaaac 900
tgtgatcatg ggaagctta aattgggtca ataacacgca tcaagttggt tatttcctgg 960
gctacatacc ttggatagat 980

SEQ ID NO:10,481: Template LS 1076101.8 HERV amino acid sequence

(see, Example 11)

Met Asp Ser Arg Gly Ser Pro Leu Gly Gly Leu Gly Leu Pro Cys Gly
5 10 15

Ala Ser Leu Arg Arg Thr Pro Ala Ser Pro Ser Asp Ala Ile Gln Arg
20 25 30

Ala Leu Pro Gly Arg Lys Leu Pro Arg Trp Asn Ala Ser Pro Glu Gln
35 40 45

Arg Val Ala Val Pro Cys Gly Gly Leu Thr Gln Trp Leu Asn Thr Gly
50 55 60

Lys Glu Leu Ala Leu Gly Val Arg Thr Ser Glu Thr Cys Arg Leu Gly
65 70 75 80

Ala Val His Gly Trp Glu Gln Leu His Gln Pro Leu Gln Ser Asp Ser
85 90 95

Glu Glu Asp Asp Lys Pro Cys Ser Ser His Thr Arg Lys Leu Thr Gly
100 105 110

Pro Arg Thr Ala Glu Ala
115

SEQ ID NO:10,482: LS-1452 with His tag nucleotide sequence (see, Example 13)

atgcagcatc accaccatca ccacgtgtca caatctacag tcaggcagga ttccctgtg 60
gagccctggg aagggtatcg cgatcactct ggcattattt atggttcgcc cagactcctg 120
aacactgacc atccctctt ccaatttagac atcaggctca tgaggcacaag agctgtctgg 180
attaacccccc aggatgtca gcaacagccg caggacttgc aatctcaggt gccagcagca 240

gggAACAGTG GGACCCATTG TGTGACAGAT GCTGCCTCTC CCTCAGGGCC TTCACCTTCG 300
 TGCCTCGGGG ACTCCCTGGC AGAGACAACG TTGTCTGAGG ATACCACAGA CTCCGTTGGC 360
 AGCGCTCTC CCCATGGCTC GAGTAAAAAG AGTAGCAGCT TCTCTCTGTC CTCAACAGAG 420
 GTACACATGG TCCGCCCCAGG ATACTCTCAT CGGGTGTCTC TGCCCACAAG CCCTGGGATT 480
 TTGGCCACCT CCCCCATATCC TGAGACTGAC AGTGTCTTT TTGAGCCTTC CCACTGACA 540
 TCTGCTGCTG ATGAAGGTGTC TGTCAAGTC AGTAGAAAGA CCATTCTTC GAATTCCTTC 600
 TCACCAAGAGG TATTTGTGCT GCCTGTTGAT GTAGAAAAGG AAAATGCCA CTTTATGTT 660
 GCAGATATGA TTATATCAGC AATGGAGAAA ATGAAGTGTG ACATTCTGAG TCAACAGCAG 720
 ACAGAGAGCT GGAGTAAAGA AGTCAGTGGG TTACTTGGGA GTGATCAGCC TGACTCTGAA 780
 ATGACTTTG ATACCAACAT AAAGCAAGAG TCTGGGTCTT CTACTCTTC ATACAGTGGC 840
 TATGAAGGTT GTGCTGTGTT ACAGGTCAGC CCAGTGACTIONG AAACACGTC AAACACGTC 900
 GTGAAAGAGA TTTGCAAATG CGATGTTGAT GAATTTGTTA TTTTAGAGCT TGGAGATTT 960
 AATGATATCA CAGAAACCTG TAGCTGTTCC TGCACTCTC CTAAGAGTGT CACTTATGAG 1020
 CCAGACTTC ATTCTGCAGA ACTATTAGCC AAAGAGCTGT ACCGCGTGT CCAGAAGTGC 1080
 TGGATACTGT CAGTAGTTAA TTCTCAGCTG GCAGGTTCCC TGAGTGCAGC TGGCTCGATA 1140
 GTCGTAATG AAGAGTGTGT CCAGAAAAGAC TTGAAATCCA GTATGAATGT AGTACAGGAA 1200
 ATTAAATTA AGTCTAGGAT CAGAGGGACT GAAGACTGGG CTCCCTCTAG ATTCAAATC 1260
 ATATTAATA TTCAATCCACC ACTCAAGAGG GACCTTGTGG TGGCAGGCCA GAATTTTC 1320
 TGTGCCGGCT GTGGAACCTC AGTAGAGCCT AAGTTTGTGA AGCGGCTCCG GTACTGCGAA 1380
 TACCTAGGGA AGTATTCTG TGACTGCTGC CACTCATATG CAGAGTCGTG CATCCCTGCC 1440
 CGAACCTCTGA TGATGTGGGA CTTCAAGAAG TACTACGTCA GCAATTCTC CAAACAGCTG 1500
 CTGACAGCA TATGGCACCA GCCCCATTTC AATTGCTGA GCACTGGCCA AAGCCTGTAT 1560
 GCGAAAGCCA AGGAGCTGGA CAGAGTGAAG GAAATTCAAG AGCAGCTTT CCATATCAAG 1620
 AAGCTGTTGA AGACCTGTAG GTTTGCTAAC AGTGCATTAA AGGAGTTCGA GCAGGTGCCG 1680
 GGACACTTGA CTGATGAGCT CCACCTGTTCC TCCCTTGAGG ACCTGGTCAG GATCAAGAAA 1740
 GGGCTGCTGG CACCCTTAAC CAAGGACATT CTGAAAGCTT CCCTTCACAA TGTGGCTGGC 1800
 TGTGAGCTGT GTCAAGGAAA GGGCTTTATT TGTGAATTTT GCCAGAAAC GACTGTCATC 1860
 TTCCCATTTCA AGACAGCAAC ATGAGAAGA TGTTCAGCGT GCAGGGCTTG CTTTCACAAA 1920
 CAGTGCTTCC AGTCCTCCGA GTGCCCGG TGTCGAGGA TCACAGCGAG GAGAAAACCTT 1980
 CTGGAAAGTG TGGCCTCTGC AGCAACA 2007

SEQ ID NO:10,483: LS-1452 with His tag amino acid sequence (see, Example 13)

Met	Gln	His	His	His	His	His	Val	Ser	Gln	Ser	Thr	Val	Arg	Gln
							5					10		15
Asp	Ser	Pro	Val	Glu	Pro	Trp	Glu	Gly	Ile	Ser	Asp	His	Ser	Gly
							20					25		30
Ile	Asp	Gly	Ser	Pro	Arg	Leu	Leu	Asn	Thr	Asp	His	Pro	Pro	Cys
							35					40		45
Leu	Asp	Ile	Arg	Leu	Met	Arg	His	Lys	Ala	Val	Trp	Ile	Asn	Pro
							50					55		60
Asp	Val	Gln	Gln	Gln	Pro	Gln	Asp	Leu	Gln	Ser	Gln	Val	Pro	Ala
							65					70		75
Gly	Asn	Ser	Gly	Thr	His	Phe	Val	Thr	Asp	Ala	Ala	Ser	Pro	Ser
														Gly

	85	90	95
Pro Ser Pro Ser Cys Leu Gly Asp Ser Leu Ala Glu Thr Thr Leu Ser			
100	105	110	
Glu Asp Thr Thr Asp Ser Val Gly Ser Ala Ser Pro His Gly Ser Ser			
115	120	125	
Glu Lys Ser Ser Ser Phe Ser Leu Ser Ser Thr Glu Val His Met Val			
130	135	140	
Arg Pro Gly Tyr Ser His Arg Val Ser Leu Pro Thr Ser Pro Gly Ile			
145	150	155	160
Leu Ala Thr Ser Pro Tyr Pro Glu Thr Asp Ser Ala Phe Phe Glu Pro			
165	170	175	
Ser His Leu Thr Ser Ala Ala Asp Glu Gly Ala Val Gln Val Ser Arg			
180	185	190	
Arg Thr Ile Ser Ser Asn Ser Phe Ser Pro Glu Val Phe Val Leu Pro			
195	200	205	
Val Asp Val Glu Lys Glu Asn Ala His Phe Tyr Val Ala Asp Met Ile			
210	215	220	
Ile Ser Ala Met Glu Lys Met Lys Cys Asn Ile Leu Ser Gln Gln Gln			
225	230	235	240
Thr Glu Ser Trp Ser Lys Glu Val Ser Gly Leu Leu Gly Ser Asp Gln			
245	250	255	
Pro Asp Ser Glu Met Thr Phe Asp Thr Asn Ile Lys Gln Glu Ser Gly			
260	265	270	
Ser Ser Thr Ser Ser Tyr Ser Gly Tyr Glu Gly Cys Ala Val Leu Gln			
275	280	285	
Val Ser Pro Val Thr Glu Thr Arg Thr Tyr His Asp Val Lys Glu Ile			
290	295	300	
Cys Lys Cys Asp Val Asp Glu Phe Val Ile Leu Glu Leu Gly Asp Phe			
305	310	315	320
Asn Asp Ile Thr Glu Thr Cys Ser Cys Ser Cys Ser Ser Lys Ser			
325	330	335	
Val Thr Tyr Glu Pro Asp Phe Asn Ser Ala Glu Leu Leu Ala Lys Glu			
340	345	350	
Leu Tyr Arg Val Phe Gln Lys Cys Trp Ile Leu Ser Val Val Asn Ser			
355	360	365	
Gln Leu Ala Gly Ser Leu Ser Ala Ala Gly Ser Ile Val Val Asn Glu			
370	375	380	
Glu Cys Val Arg Lys Asp Phe Glu Ser Ser Met Asn Val Val Gln Glu			
385	390	395	400
Ile Lys Phe Lys Ser Arg Ile Arg Gly Thr Glu Asp Trp Ala Pro Pro			
405	410	415	
Arg Phe Gln Ile Ile Phe Asn Ile His Pro Pro Leu Lys Arg Asp Leu			
420	425	430	
Val Val Ala Ala Gln Asn Phe Phe Cys Ala Gly Cys Gly Thr Pro Val			
435	440	445	

Glu Pro Lys Phe Val Lys Arg Leu Arg Tyr Cys Glu Tyr Leu Gly Lys
 450 455 460
 Tyr Phe Cys Asp Cys Cys His Ser Tyr Ala Glu Ser Cys Ile Pro Ala
 465 470 475 480
 Arg Ile Leu Met Met Trp Asp Phe Lys Lys Tyr Tyr Val Ser Asn Phe
 485 490 495
 Ser Lys Gln Leu Leu Asp Ser Ile Trp His Gln Pro Ile Phe Asn Leu
 500 505 510
 Leu Ser Ile Gly Gln Ser Leu Tyr Ala Lys Ala Lys Glu Leu Asp Arg
 515 520 525
 Val Lys Glu Ile Gln Glu Gln Leu Phe His Ile Lys Lys Leu Leu Lys
 530 535 540
 Thr Cys Arg Phe Ala Asn Ser Ala Leu Lys Glu Phe Glu Gln Val Pro
 545 550 555 560
 Gly His Leu Thr Asp Glu Leu His Leu Phe Ser Leu Glu Asp Leu Val
 565 570 575
 Arg Ile Lys Lys Gly Leu Leu Ala Pro Leu Leu Lys Asp Ile Leu Lys
 580 585 590
 Ala Ser Leu Ala His Val Ala Gly Cys Glu Leu Cys Gln Gly Lys Gly
 595 600 605
 Phe Ile Cys Glu Phe Cys Gln Asn Thr Thr Val Ile Phe Pro Phe Gln
 610 615 620
 Thr Ala Thr Cys Arg Arg Cys Ser Ala Cys Arg Ala Cys Phe His Lys
 625 630 635 640
 Gln Cys Phe Gln Ser Ser Glu Cys Pro Arg Cys Ala Arg Ile Thr Ala
 645 650 655
 Arg Arg Lys Leu Leu Glu Ser Val Ala Ser Ala Ala Thr
 660 665

SEQ ID NO:10,484: TCL-1 with His tag nucleotide sequence (see, Example 13)

atgcagcatc accaccatca ccacgcccag tgcccgacac tcggggaggc agtcaccgac 60
 caccggacc gcctgtggc ctgggagaag ttcgtgtatt tggacgagaa gcagcacgccc 120
 tggctgcctt taaccatcga gataaaggat aggttacagt tacgggtgct cttgcgtcgg 180
 gaagacgtcg tccctggggag gcctatgacc cccacccaga taggcccag cctgctgcct 240
 atcatgtggc agctctaccc tcatggacga taccgatcct cagactccag tttctggcgc 300
 tttagtgtacc acatcaagat tgacggcggtg gaggacatgc ttctcgagct gctgccagat 360
 gactgatga
 369

SEQ ID NO:10,485: TCL-1 with His tag amino acid sequence (see, Example 13)

Met Gln His His His His His Ala Glu Cys Pro Thr Leu Gly Glu
 5 10 15
 Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala Trp Glu Lys Phe Val
 20 25 30

Tyr Leu Asp Glu Lys Gln His Ala Trp Leu Pro Leu Thr Ile Glu Ile
 35 40 45
 Lys Asp Arg Leu Gln Leu Arg Val Leu Leu Arg Arg Glu Asp Val Val
 50 55 60
 Leu Gly Arg Pro Met Thr Pro Thr Gln Ile Gly Pro Ser Leu Leu Pro
 65 70 75 80
 Ile Met Trp Gln Leu Tyr Pro Asp Gly Arg Tyr Arg Ser Ser Asp Ser
 85 90 95
 Ser Phe Trp Arg Leu Val Tyr His Ile Lys Ile Asp Gly Val Glu Asp
 100 105 110
 Met Leu Leu Glu Leu Leu Pro Asp Asp
 115 120

Sequences Listed in Figure 5- Highly expressed in lymphoma cells

SEQ ID NO: 10,486

gtgaaacacc ctcggccggg aagtcaagttc gttctctcct ctcctctctt cttgtttgaa 60
 catgggtcgcc actaaagcag acagtgttcc aggcacttac agaaaagtgg tggctgctcg 120
 agccccccaga aaggtgcttg gttcttccac ctctgcccact aattcgacat cagtttcatc 180
 gaggaaaagct gaaaataaaat atgcaggagg gaaccccggtt tgctgtgcgc 240
 gtggcaaaaaa ggaatttggag aattctttag gttgtcccct aaagattctg aaaaagagaa 300
 tcagattcct gaagaggcag gaagcagtgg ctttagaaaaa gcaaagagaa aagcatgtcc 360
 tttgcaacct gatcacacaa atgtatggaaa agaatagaac tttcttcattc atctttgaat 420
 aacgtctcct tggtttaccct ggtattcttag aatgtaaaatt tacataaaatg tgtttggcc 480
 aattagcttt gttgaacagg catttaatta aaaaatttag gttt 524

SEQ ID NO: 10,487

ctgcttgtac ttcaaagccc tccgtcttagc catctcagcc aggctcaggt tccttctccc 60
 acccatcagg ccaagcagga cttgtcaaac atacacattc aagttccctag cacacagtag 120
 gtgctaagtg ggaatttgatt ataaaacttga attcttccat caacaaatat ccacctctcc 180
 tgtccagctt gcctcagatc ttccagggttct ctcttctctg aggccagctaa gcttctacat 240
 ctttcatgaa gtttccctta cttctcgaca gaagacagtt ccctttagg 289

SEQ ID NO: 10,488

ccattagctc ctgttagctag ttccctgtctt ttccaaaacc tgttttttt ttggctttt 60
 ggttagatgct gtggctctct tatggcctcc aataaaacata agtgaggcag agttggttc 120
 tattgtttgc aaccaacgaa cttaatggat tctgtattag aaagaactgg tatatttctt 180
 taagcaaaga ctaggactct atggggctca acaaaactctg taatgcctt tccactcccc 240
 tgacaaaat aaatataattt gttactgctg aaacgcaaat tatccccaaa ccaagtagct 300
 tt 302

SEQ ID NO: 10,489

tataaaactgt ggcgggatag ttttcgggtc cttgtccagt gaaacaccct cggccggaa 60
 gtcagttcgat tctctcctct cctcttctt tgtttgaaca tggctgcggac taaagcagac 120
 agtggccatc gcaacttacag aaaagtggtg gctgtcgag cccccagaaa ggtgcttgg 180
 tcttccaccc tggccactaa ttgcacatca gtttcatcga ggaaagctga aaataaaat 240
 gcaaggaggga accccgtttg cgtgcgc 300
 ttcttttaggt tggccctaa agattctgaa aaagagaatc agattccctgaa agaggcagga 360
 agcagtggct taggaaaaggc aaagagaaaaa gcatgtccctt tgcaacctgaa tcacacaaaat 420

gataaaaaaag aatagaactt tctcattcat ctttgaataa cgttccttg tttaccctgg 480
tattctagaa tgtaaattta cataaaatgtg tttgttccaa tttagtttg tgaacaggca 540
tttaattaaa aaattttaggt tt 562

SEQ ID NO: 10,490

ctgcttggac ttcaaagccc tccgccttagc catctcagcc aggctcaggt tccttctccc 60
accatcagg ccaaggcagga cttgtcaaac atacacattc aagttcctag cacacagtag 120
gtgctaagt ggaattgatt ataaaactga attcttccat caacaaatat ccacctctcc 180
tgtccagctt gcctcagatc tttaggttct ctcttctctg aggtagctaa gcttctacat 240
ccttcataaa gtttccctta cttctcgaca gaagacagtt cccttttagg 289

SEQ ID NO: 10,491

aaaaaaaaacaa aacaaagcaa agcaaagcaa aacaaaacag ctctttataaa tggataatgg 60
cttaagcaaa tcgctttagt ttttttcta ttttaagattt aggacagact actcgctcaa 120
aattcactat ttacagagaa ggtccttaggg aacaggataa ctatatttagg tttagctctc 180
ataatacaat atccataatg gctttagaag aatgtaaata aataacattg gtaaacagcg 240
tatactgata ttttctgaca aactcattta tctaacatca tgctgagcaa tcaagaggat 300
tcctctatata tttt 315

SEQ ID NO: 10,492

aaaaaaaaaaaaa tcaaaagcag acatgtttgg ctgaaataaa accaagaaaac acagctaaaa 60
ctccccccata aacctaaaag tccatggaga attcaattc tcatttccat tcagaaatct 120
ggctacaaag tgatttggg gctatttggg acgtacaga gtgctgaaag aaaccagct 180
ctttagtctc ttagatccc tccctgttagga agtgggtggg aagccagcgg accatggca 240
agtcaactcc tggctacttg gcaggagtc agactgtgct ctctccattc cccaggactc 300
cacagaacca tctggtaactg ctgtgctgg gtgaacagtg agagcagatg ccacaaaacg 360
cagagaacca gaatgtgacc gcaaggagcc aggaccttgc gcttttcat ggattacaaa 420
tctagggcca aggagaggaa aagcagaaaag agccctattt ggaagaggag ctggctgcgc 480
ccctaaactg agatggaaag agtaaggctc ttgagccac acctgg 526

SEQ ID NO: 10,493

ctgggcana ccaagtcaca gtttccagcg tgctgctcag ccctccgagt gtgtgtgctc 60
atcctttca tagaagtccc atmkgscatg gagagggttgg ggcgtcarag ctgwgtattgc 120
cagaggccct tccttgagaa ctgtggggaa ggaggccctg ggggtttctt ctgttaggcag 180
agctcaggcc ccagtccaccc ctggccaccct cagcctggca ctgttgcggc agagcctctg 240
ctgcctctct cttecttaccc atctgcagac cagcagaata ttctccccct ctcacatccca 300
accaggagtt tgggtgtggg tctggacacg gccagagcag tcactgcggg gctgggtttg 360
ctgggcttcc ctgtcaaagc aatgctaacg tccagctctc gactcaaggc caggttcttc 420
tcccacttgt ggcctttgg gcttggaggc tgagccaggc gctcctctcc tgctggccgt 480
ccaggaacag acatcttcac atcctcagtc ttccaaaccc ggaccatgccc gtcttgactc 540
ccggtgatga tggatctggct tggatctggct gctggccct ccatcaggca gcaacaggtt 600
atggctcctt ctggggccca ggctgtggtg atgctgg 637

SEQ ID NO: 10,494

aaacaatgct acactcattt ttggcaaagt gctgtattgt tcagtctgtg tacaactg 60
accatctatg aaccaatcg tataaaaaat ttctataaaa acaaattta gacagtggct 120
caagaaaaca agctgcccatt tatgcataga ttgtatgtaca gtaacctaac caaatgtccc 180
tttgaattt tcaagttact gaaaaaaaat gtgtcgagaa acacattaag aaggcacatg 240
tacagtctac aatactcttc agtctcccta actcatgccc tgcccctata aaggaaatat 300
gttcacaatt ttacttgaga aaaaaaaaaca aagccactta aaaaaaaaaa acacacacgc 360
aatttattaaa gttcaaaaatc tctggaggaa aatacaagca aaaccactca tacactccaa 420
gcctgaaaca cacatctaac ctccccaggt actgggttgg tttcagagg tccacactana 480
aaacaaataac taaaacttca ggcaaaacag agcaaaactg gacatttaac aattacacaa 540

SEQ ID NO: 10,495

ctgaataggc acccaaagt ccgtgactaa atttcgttg tcttttgat agcaaattat 60
 gttaagagac agtgatggct agggctcaac aatttgtat tcccatgtt gtgtgagaca 120
 gagtttgtt tcccttgaac ttggtagaa ttgtgctact gtgaacgctg atcctgcata 180
 tggaaagtccc gttcggtga catttcctgg 210

SEQ ID NO: 10,496

cctcctcgac caaggcaggg aacttcaatc tgtataagta tctgcagtt ctggaataat 60
 ttgaagaccc catggagcta aggagattaa gtggaggatt ttcattgtt cagagggca 120
 aggggcaat ccattgctaa ttctttaatg atgaaaaatg gtaagaagtt gttaaactcc 180
 tttggggatt taaaaaagtgt atacgtaaac agaagagaga gagagagaga gaaatcacag 240
 tagtgaggct aacaaaata atgataaaaaa ggtagaaga acccaggata cttagtggat 300
 gcctagacaa cataaaaata gatttataga aggaagcaat ggaatttcaa tataaaagg 360
 tatcagaaag ttaatgtgtt gcatctgaaa ttcaaagtat ttcttttgg ctacacaaga 420
 aagacttttta ataaaaccct ttgtatataat ttctgaaagg naaatatttt ataggaaat 480
 ggaggattgg aagaaaatct gttccatcat gtctgggtat tagaattttg cttataact 540
 tgccaaaata ttacgcttcc aaggcctatg gcattatgtg tgtacccaat taaag 595

SEQ ID NO: 10,497

ctgtggctgt ctgtcagaga agcacatttt tctgcagata attagaatgg cttccccat 60
 ctctcacgga ctgtcccaag tctagaaaag aattgagttc ctcttctatt agtcaaataa 120
 aagggaaagag aatgtttgtc ttctttccct ttctgtatgt ttaagaaaat aaacgaactt 180
 aatgattcta aattatcagt gagcttaaca ctgtactata gaccaagat tacctttca 240
 aaaaagtccct tgaggtgaaa tattttgtat acgtaataca tagatgcaca tataaacaca 300
 cacatataaga atctcaatat tttaacactt ctttggtag ttgtactaac tcactaaccc 360
 tgagggaaaaa gttaagaaat tgaaagtgtt ttcttcaaaa gttgagatt aacaataaaa 420
 ggtgttactt tgataactaa aaggaacttt attatcctct tcctaaaata aaccaatgcc 480
 tattctgaaa atggcacttg caattacaat ttgcattat caaagctacc actgaggtag 540
 aggcattatc taaaacaaat accacttac atttattggc agttacctcg agagagaccc 600
 atacaccatc ttctagcaga gcacagtcaa tcaaattacc ttccggtaaa gctatagcat 660
 gtctagtcgt ttgacagata taaaagggtgg tcataaaaga aacataaacc ataggctgtg 720
 ctccaaaggc atattgg 737

SEQ ID NO: 10,498

ctgtacgtta caagttggc cattttgaag cttgacattt tagttgcca ttatgttaaa 60
 aacatctaaa taggtgttag ttctcagga gtagattgtt agtgttgact ttccctgtaa 120
 agcagacatc gttcttggcc tgccctgcat tgtatactag atttcattgt tgcctctcat 180
 gcttcttgcgt ttgcttcatg gtttatgctc gccatggaaa gctatcgat acagttcat 240
 gcttataccca aagaattaaa tctgatcttt aatatctgtat attttcctgg tactcgact 300
 gataagggat tattgaaagt cagtcacaga atttggaaat aaattctgtt ctctccttag 360
 ctatttgcgtt ctttccatg aggccaaagaa ctcattgcaa aacatttttgcgtt caaggatgaa 420
 tgcctgtatt tggctcttagga acagtcattt ttgtctgtat tttagaattac tggtagctt 480
 ttttaaagca agaaaaagca g 501

SEQ ID NO: 10,499

ccacaagctc tttagatggc tacttttagt aaactcttca ttcatcctgg cattttgaa 60
 aatattcgtc aaacatagag gaagactcat cttcacgttc ctttgggttct taaaattctaa 120
 ggtcttctcc atattgaaatg gcaaaatcaa tatgctgcaa tacaatgttc atgcttctt 180
 catctgactg atcgtaaggt aaaaatcgaa ccatgctgtat gtcataatc agtccacata 240

tagcttagt cagttcttg aatttttgc ttcttaagtc actttagaa tcttctaata 300
aagaatacat gtctgatct aaaaatttct caatttcctt tttgtttt ttactcagca 360
gatccatccc tgtcatgtat ttgacttgcg gaatttctag agagatcatg gcactcaggg 420
ctgccaagat gccagaaata aacttgaatg actccaccat gaactgagaa tcaacaagaa 480
aaactccaca gactcggAAC tcccactgct cgagctgctg gaccagct 528

SEQ ID NO: 10,500

actaaacagc caatcatggc attcaaaggc caccgtaaag cagtcttta tgcaaagttt 60
gtgagtggtg aggaattgt ctctgcctca acagacagtc agctaaaact gtggaatgta 120
gggaaaccat actgcctacg ttccctcaag ggtcatatca atgaaaaaaa cttttaggc 180
ctggcttcca atggagatata tagcttgcg ggaagtgaaa ataactctc ctacctgtac 240
tataaaggac ttctaaagac ttgcttaact tttaagttt atacagtcaa aagtgttctc 300
gacaaagacc gaaaagaaga tgatacaaat gaatttgcg gtcgtgtgt ctggagggca 360
ctaccagatg gggagtcgg tgcgtgtt gctgctaaca gtcagggtac aattaagggt 420
ctagaattgg tatgaagggt taactcaagt caaattgtac ttgatcctgc taaaatacat 480
ctgcag 486

SEQ ID NO: 10,501

cctccctgc agctctctgt gtytgtgatg atggagctgg gttggggaaa tcctgctgtg 60
acatttgccc tgacgcagtt cccgcacagca tggtgcttc caagctatgc tcttgatggg 120
caccgcgtaaag gagcttctac atgcatttgcg gatggagcct ctcctatctt tgcaagcctt 180
tgtggttctt ccctttaat ctgcatttca cggacccaa caggagaata atttggtctt 240
cagtttgctc tggttttagac aaatacttca catgactgtat gtaaactgtt gcatagtttc 300
acaaaaggctt tctcattcat tcctgaaatt ctccatcagt cacaacaca aattgttcag 360
tatctgggaa attcaagcc ctttcctca aacagacatt tctccttattc attcttcctt 420
caggggaagt attgaaagtc attgaaagtc atccccaccc actagaggag agaaangcaa 480
gccccagaaaaa ggcaagaggt acacaggcc cc 512

SEQ ID NO: 10,502

ctgcttctga ttgcacccaa aatggcacc accaaaaaaa acacaaccta tgcgggttc 60
ggatttttaa gaagtattt cagttaaatc gacactaaag tacaattata cttggcttct 120
tgtggcataa atgatcttgc attttaaatc cattttgcg ttaccttattt agaacaaaac 180
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SEQ ID NO: 10,503

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SEQ ID NO: 10,504

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218

SEQ ID NO: 10,505

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SEQ ID NO: 10,506

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SEQ ID NO: 10,507

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SEQ ID NO: 10,508

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SEQ ID NO: 10,511

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SEQ ID NO: 10,512

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SEQ ID NO: 10,513

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SEQ ID NO: 10,514

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SEQ ID NO: 10,515

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SEQ ID NO: 10,516

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SEQ ID NO: 10,517

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SEQ ID NO: 10,518

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SEQ ID NO: 10,519

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SEQ ID NO: 10,520

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SEQ ID NO: 10,521

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SEQ ID NO: 10,522

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SEQ ID NO: 10,523

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SEQ ID NO: 10,524

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SEQ ID NO: 10,525

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SEQ ID NO: 10,526

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SEQ ID NO: 10,527

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SEQ ID NO: 10,528

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SEQ ID NO: 10,529

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SEQ ID NO: 10,530

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SEQ ID NO: 10,531

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SEQ ID NO: 10,532

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SEQ ID NO: 10,533

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tgcattgtaa aatgagagaa ttttcaaata atgcaattac tctatggat tctgttttaa 540
tagtaatata cccatatgaa gcaggatata tgagaataaa ttttgcctcat aacaattct 600
gaaatctgaa gttttgggttc tgctgttataa gtatgaattc gcttt 645

SEQ ID NO: 10,534

ccaatcatag agatatactgc accggcctgc aaagcttcca tgaacgcttt ggtcccagac 60
ttggcgatag taccaagggtt attgtatcaag tcagccttgg tcattccaat tccagttatcc 120
acaatagtga gagttcgatc ttgtttgttc ggtataagggt taatatgcag ctctttccca 180
gagtcataatt tactggatc tgcataaggctt tcataccgga ttttgcctaa tgcatctgat 240
gaattttgaaa tgagctctc cagaaaagatc tcttgcgttsg agtagaaaagt attgatgatc 300
aatgacatca actgggcaat ttctgcctga aaggcgaacg tctcaacctc ctccctcc 360
atcggttggt ctgggtctg gtttgcctca ggcattttgg ctaagtgacc gcacaggacc 420
aacggcacag cc 432

SEQ ID NO: 10,535

ctgacatgct ctcagggggtg aagaagttt a gcttaaaaata cctgatggcg ctgcataaac 60
tggggatttg ggaactgagt ttttagctct gtgacacaca acataaaaaaa caaaaatcca 120
gtctcattag ctaaattccgg attaaaatct gaaatgtttt tatggagttg ccaacaggct 180
ggaatgtacc tgatacagtt taatctgctt ttatttctt ggctgtcttc caaaccactt 240

tcttcctgta attcttaagt tggctagtcc tccttcctca gaaaaattac ccctaagaat 300
cttcctaata gtgagggtgt acttccgaat agaagagtcc ttccggctgaa atggcatctc 360
caagg 365

SEQ ID NO: 10,536

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gtatTTcaa gaacaataaag atagataaca gcattaaagc ataatcctt aagaattcat 120
gagaaaaaaa ggatgataaa acttaagctt ctttttcaga tgTTTaaaaaa ttcttataaa 180
atttttgc ccaagatcaa tcatataacc atggtacata aaatatgcta actacattgc 240
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agcatcactt tcgtctacta gttggtaatc ctgttccatt tccgtagga agccactccc 420
agatcctgrc cagagcckga gccggagccg aagcctgatc cagagtagtc ctcakaaagt 480
ggaaagatac gattcaagtc ctggattmtc gc 512

Sequences Listed in Figure 6-Highly expressed in lymphoma cells

SEQ ID NO: 10,537

aaatatgaat ttgtcttaaa ggcaattcct ttttgcttct gtattatctg gaaaagcatg 60
agagaggcga cacctcaaca aactgatcg agaaaataag cagttactac cctgataggc 120
accttccaa tcctgttgct tttgaccatt gtctgtccaa cggacacacc tcaaacaac 180
aaaactacca aatagatgac agatcagaat aaaggtgaga ggtctggtcc ccattgaagg 240
ctgctacagt cttcaaaagag gtgaaggagt tcataagaga acaacagtag gaaagtttag 300
agccaagggtt aggagaktg cccaaaagac ttcccctact acttttaggtt actgaaaact 360
caaaggatca gctacagctt tatctaagta ttactaaat gctacatgag ggtgtccctg 420
tccagtttc tggcacatga gtcctgtgtg gagagttacc tcctcttcca gggactgtgc 480
tgttggaaac ttggggcaag tcacttacct ctttgcgtt caatttctgt ataataatttc 540
taagctacct cactgagggtg gtatgaagat tcactaatgt atgtggcgtg tttgtcaatc 600
ctccagtgaa aagcactatc tagatcacat ttggatcac attagccaaa tgcagtaaat 660
gg 662

SEQ ID NO: 10,538

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atgcatggaa ttatTTcaa gacccgggt atgtggctg tgggggttgc tctccctgt 180
attatggact gagatactca ttttagtccata ataagaccag agaagtagatc tgcagatc 240
gtggggaaacg gctgcacac tcactgtctt gtgcacatgtt cttcccgagg gcattttcag 300
atttctgcca cggaggggat gctctcgcg aaggggagagt caggatcatt ggaggattca 360
ttgctgtgg 369

SEQ ID NO: 10,539

ctggcatcat ctgagtctt gaaatgcttt cttgtttgtt atctgaaaaa agcttaggtgg 60
cctttttagt atcaaatttc aatcttggcc tcactggaaac catgctctac agagcttcc 120
caacagttta gcaagtaagc aaaatcagct ttgtcttcc atatttcgta ggtgagactg 180
gggctttt 188

SEQ ID NO: 10,540

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tgtgaagatg gctgcagttt tgataccctt atcttcattt tgcgttgcctt gaaggaatga 120
accaactgtt gacaacattt gtttgactac gaattgacaa cgttctttc tagatggcaa 180

ggtaagtgtt accaaggaa ggcctatgtct ataattaact gttatttcat cag

233

SEQ ID NO: 10,541

aaataaaagtg gttacattca aactttaact tccttagtac catgctgcag atttcagcac 60
tgttaaggta ttgcagaagaat gccccaccct ctgggtctg atcatgtatc tagcaacatt 120
gcagtagaa gaaaagagat gccccggctc cagccatgg actagttaat acagtgaagc 180
aggttcctgt cttttaccct tcctgctcag aacataaaaag attaaggact aaaatcaagg 240
aaggctggaa gtttttagagc tggcaaaaatg aagtctaaaa gataatcaa ggcaaaacaaat 300
tactgagaac ttggctgtt cttaacctgg caagtctaaa agccttctt taaccttgta 360
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ttatttacaa atcttgcatac aaatacttct ggagggaaaa gagaaaaagaa ttcaactaagt 480
tccanaagac aaagctntaa ttgcagacg tatacaaac 519

SEQ ID NO: 10,542

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ccacataaaa tttcatcaga aagtggaaact tgattacagc ccaaactaga caaggcaatt 180
caggtgcccgg gaccccgaaag tccacgtgag actacaggag aacgtgcatt atggtgctt 240
ccagccagtc tcttgaggaa ctgcctgtaa cggtcacggt tgggggaga aacaactcca 300
tttttttaa gttttttttt ttatggatt aaatataatg cttacgttcc ttggcattt 360
tgtccaaaca gacttcgaca tatgaagtgg ggacataacc ctcttcattt tcatttctcc 420
gaatgcgggt ccagccatcg ccttgcattt cctctatgac atacaatgtt tctccttcaa 480
ctacggaaat cgttccttca ttctgacctt caaatgtgta gagagcttg cacgtcccta 540
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SEQ ID NO: 10,543

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cttcaattc tatatattga gagatggaa gagtatatca gagatattt tggaaaggag 240
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tt

SEQ ID NO: 10,544

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atgctgtat gcccattt acaagcgatt ttaattactc tcatttataatg gaaacaagtc 180
cccagaaaa gaaaaagaag aaaaatgata cagcaaacca tctgaagcaa tccaagtcc 240
atgcctacag tgacccaggt ctactttgc tgaagagaac actggtaactg cattcaaaacc 300
acaacagaat ccgtcaacta actgacctt ctgaattaaa ctgaggtatg aatcaattt 360
aggtatgaac agggaaaggca aaatgcaata ccagattatg aaaataacca aaatggaaaa 420
atttgatgtt gaagatatgt ggcttggatt gctccacatc tttgtttaaa acatattaag 480
aaaaggcttt aattacatct gtagtctgaa gcattctaa acacaccagt attccagcaa 540
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SEQ ID NO: 10,545

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atacagattt gagaatgtat gctaaatttta taggatgtt cagtaacttta aaaagctaaac 180
atgagagcat gccaaaattt gctaaatgtt acaaagatca agggctgtcc gcaacagggaa 240
agaacagttt tggaaatgtt tattttttagg taggttttgc aagcttttg 300

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ttcgagtctg agttt 375

SEQ ID NO: 10,546

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tttgagttaa agcttcataat ggtaactgca tcctgttcgg acactatagt ctaaattttt 240
gaaactgtgt ggtgttcgtc aaaagtagga ataacaacgt aaaagctaat taaggtcaca 300
aacttcagtg aaacccttaa aagtccaaat cttcttgata ttgtgaaccg tacccttcc 360
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SEQ ID NO: 10,547

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ctgtgtctgc atgcacgtgt aaatgtatgc ag 332

SEQ ID NO: 10,548

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aaagagaaat gaggactga tacatgctaa agcatggatg agccttgagc gcattttgc 120
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tccaaaatag gcaaattccat ggagacagaa agcanataaa tgggtgtaaag aagctganag 240
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aatttcacat acactttacc ataattttt 389

SEQ ID NO: 10,549

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gcttttaagt attattatag acttttggaa actcacgaaa caagcaatcc ctaaatttctc 180
gcccgaggaaa gatatggta ttaaatggtt tttgagaacc ttgagagtgt atattctatg 240
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SEQ ID NO: 10,550

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gagtgcacgc tggggcaatc ttccctggaca gccaccagag aaaggcgtca gaccccac 298

SEQ ID NO: 10,551

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SEQ ID NO: 10,552

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SEQ ID NO: 10,553

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cagg 364

SEQ ID NO: 10,555

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cacgccccat gggattacag aacacagcta cagaattagg atctcatggt aacaatgagg 240
aattaggta ctgtagaact aaaatatgtt taatgaaatt aaaatgcaat ggaaaaaaaa 300
tcaggcaaca gaacatttgc atgaatttac aggactgatt atatcccacg gcactgaatg 360
acaaacagtt ctctccata cagtcgaat tagaggcata gaagtcatc tgaatgtga 420
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agacaaaatc atcggtaaag a gtagctt 509

SEQ ID NO: 10,556

aaacagcacc agcacttctg gctggtttga accttaaatg ccaccaccca ccagagagga 60
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cagaagaaac ttatttagaaat aaggccaccc aggaatgttc ttaacttttc cattcagctt 180
ttggctgata tatgaaaata caaataaata catccttcc ccaggtgcaa ggctaaacca 240
gcagctccaa gggcttggtc tacagtgtc agaaagacac actgccttaa aagtcaggct 300
agtgccttag ctccgggtggc ctctgcaat gagg 334

SEQ ID NO: 10,557

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tttttt 546

SEQ ID NO: 10,558

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aaaatattat actctcgaa 499

SEQ ID NO: 10,559

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tacagatgtt ttaccttaag aattatttaa gttgttttgg gtttaagacag ttttcagtgt 180
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SEQ ID NO: 10,560

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SEQ ID NO: 10,561

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aatcatttt 729

SEQ ID NO: 10,562

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gataaaagtat ctggccttt ctgacaccat aatagttcat ttttaggga ataagccatt 240
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annactcta tttcatcaaa attt 384

SEQ ID NO: 10,563

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ctacaactca aaagttt 377

SEQ ID NO: 10,564

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cacacacaca ttccacacgc atcattaaag gatagccatt tattttcat cttcatcctc 180
ttccctccta tcttcatctt ctcttcctc tcattttctg gttcgttctt 240
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cccaatggat aggccagggt gttcactttt gatctttggg cgatgtt 467

SEQ ID NO: 10,565

aaagaacaga gttctggagt aaagaagcag gttccctttt cagtagacac ctcccgcttg 60
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ttcattgtt ggttggccgt caaatcgaa tntgatctgc ttcattgaca atccctgtcg 180
ttcacaatag gccttcatta gtttactaag tgggttatgc ctcttaatct taaaactgcac 240
cacagaacca tcctgccccg ccacccatcaa attaatatga tcgttgttct cagtcttgac 300
tcttccttg ggctttcgtt cggccatggc gagccggc gtctcctcag 350

SEQ ID NO: 10,566

ctgaagctgc aggtgtctgat cgagtcaaag agccctgaca tagccatgtt ttttgaagaa 60
gccttgc acctgaaacc ccagggttgc ctgcattgtt ggatttgcctg ggcagagtgg 120
agtgaagggtt cccaaaggca agaagacact gaggcagttt ttaagaaagc tctcttagct 180
gtcatacggtt ccgactcagt aaccctgaaag aataagtacc tggattgggc ttatcgaagt 240
ggtgctaca aaaaggccag agctgtgttt 270

SEQ ID NO: 10,567

ctgcctataa aactagactt ctgacgctgg gctccagctt cattctcaca ggtcatcatc 60
ctcatccggg agagcagttg tctgagcaac ctctaaatcg tgctcatact gtactgcca 120
agctgggtcc atgacaactt ctggtggggc gagagcagggc atggcaacaa attccaaatgt 180
agggtctcca atgagcttcc tagcaagcca gaggaagggc ttttcaaagt tgttagttact 240
tttggcagaa atgtcgtagt actgaagatt cttcttcgg tggaaagacaa tggatttcgc 300
cttcacttcc ctgtccttaa tatccacttt gttgccacac aacacaatgg ggatgtttc 360
acacactcgt accagatctc tatgccagtt aggcacattc ttgtaagtaa ctctcgatgt 420
tacatcaaac attatgatgg cacactggc ttggatataa tagcc 465

SEQ ID NO: 10,568

ccttgatgat accattatcc tcattataga ttagtgcacgg gcccctgcgc tggatacggc 60
gacggttct cattttgcct ttgccagctc tcatttcgt agaggcatag acctacaag 120
tgagcagtt tagtatttcg attaagatag aatctctgca atagatcttca agagttttaa 180
ttccctttta cagatgatta aactgggcac aataacttgc caaggttaca cagagccata 240
aacagcagtt aggattcaaa cccaaatgtt cgggctctga ggttcttgc ttctcacaca 300
ttaaggctta gctatactgc ccttatcttc tggaaatttca aatgtacaac tggaaacaag 360
gagtacaaa ctgtaaatgt gctcattgaa cggacccccc tgatatttca ccaggcttca 420
agtttcttaa ggagcaaaac agtttccttgc gtcttcttgc agccttcaac ttatcttca 480
actaccaaaag gaagttcagg aacttcctca atacgatgac ctttagacat gaccagtgc 540
ggtagggctg aggccagccag ggccagaacag atggcgtatc gtttttgggt tggtttact 600
cyacgatgcc aacggcgcaca ggttttgggt ggtgcaaaaca ttccggcctcc acgacacatg 660
tttccaaaag caccctgg 678

SEQ ID NO: 10,569

cgccaaatctt cgctctgagg tgctgtctca ccgggtgagac ctggaaagcgg gcgagtcgc 60
tgctgtgtcg gacctgcagc ccctggcctt ccggccaccat ggagtacctc atcggtatcc 120
aaggccccga ctatgttctt gtgcctccg accgggtggc cgccagcaat attgtccaga 180
tgaaggacga tcatgacaag atgtttaaga tgagtggaaa gatattactc ctgtgtgttgc 240
gagaggctgg agacactgta cagtttgcag aatataattca gaaaaacgtg caacttata 300
agatgcgaaa tggatatgaa ttgtctccca cggcagcagc taacttca caaccgaaacc 360
tggctgactg tcttcggagt cggaccccat atcatgtgaa cctcccttcgt gctggctatg 420
atgagcatga agggccagcg ctgtattaca tggactacat ggcagccctg g 471

SEQ ID NO: 10,570

ccacatatgc ccctgtcatc tctgctgaga aagcctacca tgaacagctt actgttagcag 60
agatcaccaa tgctgtctt gagccagcca accagatgtt gaaatgtgac cctcgccatg 120
gtaaatacat ggctgtgtc ctgttataacc gtggtgacgt ggttccaaa gatgtcaatg 180
ctgcatttc caccatcaaa accaagcgtt ccattccatgt tggtggattgg tgccccactg 240
gcttcaagggt tggcattaaat taccagcctc ccactgtgggt gcctggcggaa gacctgaaaa 300
tgttcatgaa tggggaaatg gaaacaaaatt atcaggatg gcttttgcc atgggtctta 360
tttcaccctt ctttctgtt agaaaaaaga acaatgtttt aatgtatttt t 411

SEQ ID NO: 10,571

tttttttttc caagtaagcg tctatgcagg catcacaaac tttggcggat acagtagata 60
tgtattttctt tgatgtgttcc aggtcgttcc ctaagacaaa atcaaatgtc tcaaagaatt 120
aaaagcaaaa tgcgtgtgtc ttccctggcaaa aggttccat ttgcaatgtt atctgcattt 180
ctacaaatac tcaatgttcc accggacttag agggtaaaaa accagggcag cgttccatc 240
caggggtcag ggcagaccca gagccaaaac tccatcttca gccaacattt ggaggcccag 300
cag 303

SEQ ID NO: 10,572

aaattgatct ggtgttcctt gcggggcttc aattgatct aaataratgt gagagttgaa 60
agacccataa ggggcttctc tcgcttacg atgtcttatt atttttttt cttccctctg 120
gttcatgaaa tgccagggtg aaaggatag ccaaataggc taaagcacaa gtgccactct 180
agtattcsg cagagtgcgg aataaagggtc cacgacaata ccatcacaca tccgctcg 240
gatgaacaag ggctgactga ctgataagyt cttgaaaatt ctaagctca ctgcateccct 300
tcaggtctcc aaggaatgt aagtctcctc cctgcatga gagacatgaa atgaacttag 360
tggggaga cgaaagctgg acggccctca ggggctgacc cgagggact ttggatata 420
gcagagagag ctggcatga cttattactc caagctgttag aacacggaa aatagctacc 480
ctcagccca tgcctggta actggaggac caccttagtg gaagggggac aatcagggcc 540
tctggcctgc catgtgcaca agcataacaa ttgcatttgt tt 582

SEQ ID NO: 10,573

aaagaacaga gttctggagt aaagaagcag gttccctttt cagtagacac ctcccgctctg 60
ctgttggAAC acatcaattt tatcttcattt ctccatttcc aactgtgcag gtgtgtctgt 120
ttcattgatt ggttgcctgt caaatcgaaat tctgatctgc ctcattgaca atccctgtcg 180
ttcacaatag gcttcattt gtttactaag tgggtatgc ctcttaatct taaactgcac 240
cacagaacca tcctgccccg ccaccccaa attaatatga tcgttgttct cagtcttgac 300
tccttccttg ggctttcggtt cggccatggc gagcgccgg 339

SEQ ID NO: 10,574

aaatcaataa gtaatctagg actagcatta tgggttgcgtt acctggcatt tgctcggtac 60
ataagggttca aagtttccctt tcctttttt atttattttt tattttgaa tgggtttttt 120
ccataatatt taagtttttc gatgtttaga tatttttctt cggtaagca caagtttctt 180
ttcatggtcc ctgatcaattt tt 202

SEQ ID NO: 10,575

ctgagaattc gtccgctccc gaggtgagc agggcgcccc tgagtaatg ccggcttacc 60
atcttacca tcattccgtt tagtcatcca acaagaagaa atatgaaattt ccagcaataa 120
gaaatgaaca aaagatttgg aactgaagacc taaagtgtt gcttttgcc cggtgaccag 180
ataaaatagaa ctatctgtat tatctatgca gcatgggtt ttttattttt ttacctaaag 240
acgtctctttt ttggtaataa caaacgtgtt ttttaaaaaaa gcctggttt tctcaatacg 300
ccttt 305

SEQ ID NO: 10,576

gagacaatgg ccccgatgtt atggagcccg aaggcgcatcg cagagtaac tggaaatgaga 60
ttgttgacag ctttgcgtt atgaacctct cggagttccct tctccgtggc atctacgcct 120
atggcttga gaagccctct gccatccags agcgagccat tctaccttgtt atcaagggtt 180
atgtgtgtat tgctcaagcc caatctggaa ctggaaaaac ggccacattt g 231

SEQ ID NO: 10,577

cctgcagcat gggaggttacc acgctggcag tcagcagtca caccagggtg gtcagagaca 60
ctgggtggcag catctgtgtt tgcaactgca ttcccagggt gtctgtttt tttccaaatgt 120
tctcccaataa aattccccag gagttctcc gattaaatgt cctcagggtg aaaagcatgg 180
acaccaaaatc actccgtatc cacttccatg agatgtcttg atgtccagt tcaatgatgt 240
acaatttctc aagaggctct gattagttca tttttttttttaaataa agcaccggcc cctcatcccc 300
cgtgatacag cacatctgtt aatctaggcg cctcagctaa gctgcatacg tcttagcaca 360
caggacaggt cagcggttac acatcaacac tataactatg cggcgaaact agctccccgc 420
tagccgtcaa ctactcgatgaa gactacctgtt gag 453

SEQ ID NO: 10,578

aaaacggggg ggaacggggg aacgagctgt atctatggtt cacctcattc aacttccttg 60
agtatggca ctatgatgtt gcttaattag gtaagacatg gatatttgca ccgagtgcaa 120
atactgttca taacaaggc atagctagaa agacagatgg gctcaagtgt ggacaaataa 180
tgtcatcaag gtaatagatc aaaaatatta aagccctata aaagatctga gcagtgcaact 240
ccaaaacatc cacatgacaa agtccttaaa atacaaatct cattacttctt actcatgcaa 300
ctgctaaaaa atagtgtgca gatatgtatt tatatttgcc ttaaccttca aaatctaggg 360
acataaaatct tgctttgtt aaaaaaaaata aaaaataaaaa atagacagga atttgctaca 420
ctttcccttc 430

SEQ ID NO: 10,579

ctgctgcccc tnagtnntct ttccttctcc ttttctttc ctttcttctc tcttgtgcat 60
tcttcaggc agtcatcaca ttcaaagtct tccataccca cataaccaca atgatcatgg 120
cattcaccag cagtggggct gaaaatacta tagaaatgaa catccccctg gagtccgaaa 180
tactggtatt tcgaaaataa tctccagttc atcgcagccg cctcattgtat gtattcagca 240
cagtagacta agatgactag acacagaaag ngccccgatc tgtacnctgt agctncggga 300
ggacaaggc gngaggagca cgcagagccg cgtgaaaggn gg 342

SEQ ID NO: 10,580

ttttccgcc catgttagca ttgaagttgt gagctctact tgcttgcatt tatggccctt 60
taattcaagt aattggtcag tattccgtatg ggtctttat accacccgct gggggctaaa 120
ctaatttagc tgctgctgta tacttactaa caaggaataa atgtaagct ttcttcag 180
tattgatgga tggtatctaa aagtattttt atgtttctt aacatggctt aaattttgaa 240
cttaatgtat caagttagta tggcatatt aataccctgt ctttcagat tcttcaaaca 300
cctaaatgaa agtataat taaaactga tccttttagt tcctcattat atgatatgaa 360
gggatttaact gtagcagat agtcaacctg accgtacggc atggtgctt ttttcaggat 420
aaatcttcag aaaaaaagt gcaaaacaaaa gggaaaaggg gagcaaaggg aaaacaggcc 480
gaagtggcta accaagaaac taaagaagac ttacctgcgg aaaaacggggg aacgaagact 540
gaggagagtc cagcctctga tgaagcagga gagaagaag ccaagtctga ttaataacca 600
tataccatgt cttatcagtg gtccctgtct cccttcttgc acaatccaga ngt 653

Sequences with the same tissue expression profile as CD20 and CD52 and related sequences

SEQ ID NO: 10,581 - Ly1447 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,582 - Ly1448 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,583 - Ly1449 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,584 - Ly1451 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,585 - Ly1452 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,586 - Ly1453 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,587 - Ly1454 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,588 - Ly1456 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,589 - Ly1458 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,590 - Ly1464 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,591 - Ly1480 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,592 - Ly1482 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,593 - Ly1483 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,594 - Ly1484 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,595 - Ly1485 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,596 - Ly1488 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,597 - Ly1464 full length DNA sequence

see, Figure 10

SEQ ID NO: 10,598 - Ly1464 protein sequence

see, Figure 10

SEQ ID NOS: 10,599 - 10,819 - Ly1464 MHC Class binding peptides

see, Figure 12

SEQ ID NOS: 10,820- 10,842 - Ly1464 Immunogenic portions

see, Figure 14

SEQ ID NO: 10,843 - Ly1464 - sense primer

see, Figure 15

SEQ ID NO: 10,844 - Ly1464 - anti-sense primer

see, Figure 15

SEQ ID NO: 10,845 - Ly1464 1080 bp sequence

see, Figure 16

SEQ ID NO: 10,846 - Ly1484 4141 bp sequence

see, Figure 17

SEQ ID NO: 10,847 - Ly1484 protein sequence (long)

see, Figure 17

SEQ ID NO: 10,848 - Ly1484 protein sequence (short)

see, Figure 17

SEQ ID NO: 10,849 - 10,908 - Ly1484 long MHC class I binding peptides

see, Figure 19

SEQ ID NO: 10,909 -10,968 Ly1484 short MHC class I binding peptides

see, Figure 20

SEQ ID NO: 10,969 - Ly1488 Protein Sequence

see, Figure 27

SEQ ID NO: 10,970- Ly1488 2401 bp DNA sequence

see, Figure 27

SEQ ID NO: 10,971 - Ly1456P sequence

ggtgtgcatt atgttggatg attgtaaatt ttcagtgc aaatgtaccgt gtcctaaatt 60
taaagacatg aaaaatatcc caagatcata ctagatcata atagcaattc cttaaaaaat 120
gaattatgga ggttaactgat ctctaacatgt ttcccttcatg ttgttttaat gcacaagggc 180
agaggatctg ctgacccttg gaaccagcgt gactaaccac gtgctataga cacttcatgg 240
tgtcgcaccc agggaaatca aaggcgcttg ctccctcaact gtctgtgagt cctcagccat 300
tagtacccca ccccccgcgt ctccaaaact tgagttattt caaatgtttc tcactgttca 360
tctctccact gacccactc cagaaaaggct ggagagatgc ccaagatgcc acccaccttc 420
cccaatccct cgccacagat ctgtgtctat ctcacactct gtaagtgccg ctttgc 476

SEQ ID NO: 10,972 - Alternative Ly1456P sequence

aaattnn tagga cacgg tacat tttcc actga aaattnacaa tcatcc aaca taatgc acac 60
caccctcaa aggt aacatt agtc catata caaaatcatg gaaaacctca caacatc ctt 120
ggaagg taga tattgttata tcotttacaaa aatttaatac acccattt aac 180
caaata gctc aatcgat atc aacacataag acagccaca attgtgatac agnattaaga 240
agaaactc ag gccagccg cgtc cctgtaaccc caacacttgg gggctgag 300
gcgggc agat cacctg agcc caggat tca ggaccaccc ggacaacatg gtgagacccc 360
gtctctacaa aaagtacaaa aatttagtgg gtgtggtgac ccacgcctgt agtcccagct 420
agttggagg ctaagacggg aggtatggctn gttgctttag cccaggagg t 471

SEQ ID NO: 10,973 - Ly1456P PCR subtraction library fragment

aaaataa gct atggtttcc cagtagccaa aatgatccctg caccanagct catanactga 60
gaacctganc atgcaaaanc acagtctggg tgaaggatg tctgcttgc 120
ctaattcttt gcaacccaca gtaatttggg ttctgtgaac ccacagaagc aggcccacca 180
aaaaggccct tgcgtctgtag cctggagat acatgantca ctggcggtgg gatcagtcat 240
tttttaggct gccccat tttt cctaacatgt taaaatgtgt gttctcagtc ttttcaagag 300
aggaagaagc aaagcggcac ttacagatgt tgcgtatanga cacagatctg tggcgaggga 360
ttggggaaagg tgggtggca 379

SEQ ID NO: 10,974 - Ly1451 240 bp sequence

cctaagccgc ctaaggggct gcctcggctg tccatcagtt acctcg ttc ctgagc agag 60
taattgggtg agattgtca tggaggcatt gctggctctc tagtcctgga acctac agtt 120
ggccaattc attatgcca aagg tccg tcc taggagg ttc ttgttccaag tattgagatt 180
cccgagagaa gtaggtcccc ttagatagaa gcagat ttc tcagaggtat ttagcagcag 240

SEQ ID NO: 10,975 - primer for His-Ly1452P

5' gtgtcacaatctacagtcaggcaggattctcc 3'

SEQ ID NO: 10,976 - primer for His-Ly1452P

5' gttatgttagcggccgctt atcatgttgc tgcagag 3'

SEQ ID NO: 10,977 - primer for His- TCL1

5' gccgagtgcccgacactcg 3'

SEQ ID NO: 10,978 - primer for His-TCL1

5' catttgaattcatcagtcatctggcagc 3'